5UC

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/516,992
Source: PCT/10
Date Processed by STIC: 1/23/06

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/24/05

PCT

RAW SEQUENCE LISTING DATE: 01/23/2006
PATENT APPLICATION: **US/10/516,992** TIME: 09:45:13

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

3 <110> APPLICANT: Galloway, Susan May
4 Davis, George Henry
5 Gregan, Scott Michael
6 Hanrahan, James Patrick
7 Juengel, Jennifer Lee
8 McNatty, Kenneth Pattrick
9 Mulsant, Philippe
10 Powell, Richard Patrick
13 <120> TITLE OF INVENTION: NEW GDF-9 AND GDF-9B (BMP-15) SEQUENCES FOR
14 ALTERING MAMMALIAN OVARIAN FUNCTION AND OVULATION RATE
16 <130> FILE REFERENCE: AJPARK27.001APC
18 <140> CURRENT APPLICATION NUMBER: US 10/516992
19 <141> CURRENT FILING DATE: 2004-11-30
21 <150> PRIOR APPLICATION NUMBER: PCT/NZ03/00109
22 <151> PRIOR FILING DATE: 2003-05-30
24 <160> NUMBER OF SEQ ID NOS: 18
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1879 1878 (see below)
30 <212> TYPE: DNA
31 <213> ORGANISM: Ovis aries
W--> 32 <220> **FEATURE:**
33 <221> NAME/KEY: 5'UTR
34 <222> LOCATION: (1)..(121)
W--> 35 <220> **FEATURE:**
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (122)..(124)
38 <223> OTHER INFORMATION: atg start codon.
W--> 39 <220> **FEATURE:**
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (122)..(518)
W--> 42 <220> **FEATURE:**
43 <221> NAME/KEY: CDS
W--> 44 <220> **FEATURE:**
45 <221> NAME/KEY: Intron
46 <222> LOCATION: (519)..(838)
47 <223> OTHER INFORMATION: n at 709 represents remainder of approx 900 bp unsequenced of the approx
48 1.1 kb intron
W--> 49 <220> **FEATURE:**
50 <221> NAME/KEY: mat_peptide
51 <222> LOCATION: (1396)..()
W--> 52 <220> **FEATURE:**
53 <221> NAME/KEY: misc_feature

pp 1-2, 4, 6

Does Not Comply
Corrected Diskette Needed

"n" can only represent a single nucleotide. (Per Sequence Rules)
Suggestion: delete the "n" and just state that approx 900 base pairs were unsequenced (add this)

This type of error appears in Seqs. 7 and 13

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Input Set : A:\PTO.RJ.txt
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delete - already on p. 1

54 <222> LOCATION: (709)..()
55 <223> OTHER INFORMATION: n represents approximately 900 bp of unsequenced intron.
W--> 56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (1801)..(1803)
59 <223> OTHER INFORMATION: taa stop codon.
W--> 60 <220> FEATURE:
61 <221> NAME/KEY: 3'UTR
62 <222> LOCATION: (1804)..(1879)
W--> 63 <220> FEATURE:
64 <221> NAME/KEY: mutation
65 <222> LOCATION: (1624)..(1626)
66 <223> OTHER INFORMATION: c to t at 1625 in [787] sheep changing tct serine codon to ttt
67 phenylalanine
69 <400> SEQUENCE: 1
70 gaattgaacc tagcccaccc acacacctaa agtttattta agagaccaac cgaggctctt 60
72 cctggttttt aggaagaaga ctggtatggg gaaatgtgtt ccttgctaat tcttccaagc 120
74 c atg gcg ctt ccc aac aaa ttc ttc ctt tgg ttt tgc tgc ttt gcc 166
76 Met Ala Leu Pro Asn Lys Phe Phe Leu Trp Phe Cys Cys Phe Ala
77 -315 -310 -305
79 tgg ctc tgt ttt cct att agc ctt gat tct ctg cct tct agg gga 211
80 Trp Leu Cys Phe Pro Ile Ser Leu Asp Ser Leu Pro Ser Arg Gly
81 -300 -295 -290
83 gaa gct cag att gta gct agg act gcg ttg gaa tct gag gct gag 256
84 Glu Ala Gln Ile Val Ala Arg Thr Ala Leu Glu Ser Glu Ala Glu
85 -285 -280 -275
87 act tgg tcc ttg ctg aac cat tta ggt ggg aga cac aga cct ggt 301
88 Thr Trp Ser Leu Leu Asn His Leu Gly Gly Arg His Arg Pro Gly
89 -270 -265 -260
91 ctc ctt tcc cct ctc tta gag gtt ctg tat gat ggg cac ggg gaa 346
92 Leu Leu Ser Pro Leu Leu Glu Val Leu Tyr Asp Gly His Gly Glu
93 -255 -250 -245
95 ccc ccc agg ctg cag cca gat gac aga gct ttg cgc tac atg aag 391
96 Pro Pro Arg Leu Gln Pro Asp Asp Arg Ala Leu Arg Tyr Met Lys
97 -240 -235 -230
99 agg ctc tat aag gca tac gct acc aag gag ggg acc cct aaa tcc 436
100 Arg Leu Tyr Lys Ala Tyr Ala Thr Lys Glu Gly Thr Pro Lys Ser
101 -225 -220 -215
103 aac aga cgc cac ctc tac aac act gtt cgg ctc ttc acc ccc tgt 481
104 Asn Arg Arg His Leu Tyr Asn Thr Val Arg Leu Phe Thr Pro Cys
105 -210 -205 -200
107 gct cag cac aag cag gct cct ggg gac ctg gcg gca g gtgtgtagga 528
108 Ala Gln His Lys Gln Ala Pro Gly Asp Leu Ala Ala
109 -195 -190
111 gcagattggt taatgggtgg agggaagaag aaagaccttt ttgcatttca gttacataaa 588
113 ggagttggcc ctgctccttg acttgcattt tactttgcat ggtactcaat atccaaacaa 648
115 acctggtgct tgatcttact tactgtttat tcctaatggc ctcatgggtt gatgtaggct 708
W--> 117 **natcccaccc tgacgtttaa ggcttgagaa tgtggggaga aaagggacag aagcacattc** 768
119 tgaggtactg attccttgat ttgacttcct gttacatatg gcattactgt tggattgttt 828

RAW SEQUENCE LISTING DATE: 01/23/2006
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Input Set : **A:\PTO.RJ.txt**
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```
121 ttcttctcag ga  acc  ttt cca tca gtg gat  ctg ctg ttt aac ctg  gat    876
122            Gly Thr  Phe Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp
125               -185                -180                -175
127 cgt gtt act gtt  gtg gaa cat tta ttc  aag tca gtc ttg ctg  tat      921
128 Arg Val Thr Val  Val Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr
129             -170                -165                -160
131 act ttc aac aac  tcc att tct ttt ccc  ttt cct gtt aaa tgt  ata      966
132 Thr Phe Asn Asn  Ser Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile
133             -155                -150                -145
135 tgc aac ctg gtg  ata aaa gag cca gag  ttt tct agc aag act  ctc     1011
136 Cys Asn Leu Val  Ile Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu
137             -140                -135                -130
139 cct aga gct cca  tac tca ttt acc tat  aac tca cag ttt gaa  ttt     1056
140 Pro Arg Ala Pro  Tyr Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe
141             -125                -120                -115
143 aga aag aaa tac  aaa tgg atg gag att  gat gtg acg gct cct  ctt     1101
144 Arg Lys Lys Tyr  Lys Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu
145             -110                -105                -100
147 gag cct ctg gtg gcc tcc cac aag agg aat att cac atg tct gta aat     1149
148 Glu Pro Leu Val Ala Ser His Lys Arg Asn Ile His Met Ser Val Asn
149             -95                 -90                 -85
151 ttt aca tgt gcg gaa gac cag ctg cag cat cct tca gcg cgg gac agc     1197
152 Phe Thr Cys Ala Glu Asp Gln Leu Gln His Pro Ser Ala Arg Asp Ser
153         -80                 -75                 -70
155 ctg ttt aac atg act ctt ctc gta gcg ccc tca ctg ctt ttg tat ctg     1245
156 Leu Phe Asn Met Thr Leu Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu
157     -65                 -60                 -55
159 aac gac aca agt gct cag gct ttt cac agg tgg cat tcc ctc cac cct     1293
160 Asn Asp Thr Ser Ala Gln Ala Phe His Arg Trp His Ser Leu His Pro
161 -50                 -45                 -40                 -35
163 aaa agg aag cct tca cag ggt cct gac cag aag aga ggg cta tct gcc     1341
164 Lys Arg Lys Pro Ser Gln Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala
165                 -30                 -25                 -20
167 tac ccc gtg gga gaa gaa gct gct gag ggt gta aga tcg tcc cgt cac     1389
168 Tyr Pro Val Gly Glu Glu Ala Ala Glu Gly Val Arg Ser Ser Arg His
169             -15                 -10                 -5
171 cgc aga gac cag gag agt gcc agc tct gaa ttg aag aag cct ctg gtt     1437
172 Arg Arg Asp Gln Glu Ser Ala Ser Ser Glu Leu Lys Lys Pro Leu Val
173     -1  1                   5                   10
176 cca gct tca gtc aat ctg agt gaa tac ttc aaa cag ttt ctt ttt ccc     1485
177 Pro Ala Ser Val Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro
178 15                  20                  25                  30
180 cag aat gaa tgt gag ctc cat gac ttt aga ctt agc ttt agt cag ctg     1533
181 Gln Asn Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu
182                 35                  40                  45
184 aag tgg gac aac tgg att gtg gcc cca cac aaa tac aac cct cga tac     1581
185 Lys Trp Asp Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr
186             50                  55                  60
188 tgt aaa ggg gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg     1629
```

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Input Set.: **A:\PTO.RJ.txt**
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```
189 Cys Lys Gly Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro
190         65                  70                  75
192 gtt cac acc atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca     1677
193 Val His Thr Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser
194     80                  85                  90
196 gtg cca aga cca tcc tgt gta cct gcc aag tat agc cct ttg agt gtt     1725
197 Val Pro Arg Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val
198 95                  100                 105                 110
200 ttg gcc atc gag cct gat ggc tca atc gct tat aaa gaa tat gaa gat     1773
201 Leu Ala Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp
202                 115                 120                 125
204 atg ata gcc act aag tgt acc tgt cgt taacagactc ctgtcaagta           1820
205 Met Ile Ala Thr Lys Cys Thr Cys Arg
206             130                 135
208 aaaccatgag tgtcctggcc agtgtaaatg ccgcgcccct gtctatgcct ttgggagga    1879
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 453
213 <212> TYPE: PRT
214 <213> ORGANISM: Ovis aries
W--> 215 <220> FEATURE:
     216 <221> NAME/KEY: misc_feature
     217 <222> LOCATION: (122)..(124)
     218 <223> OTHER INFORMATION: atg start codon.
W--> 219 <220> FEATURE:
     220 <221> NAME/KEY: misc_feature
     221 <222> LOCATION: (709)..()
     222 <223> OTHER INFORMATION: n represents approximately 900 bp of unsequenced intron
W--> 223 <220> FEATURE:
     224 <221> NAME/KEY: misc_feature
     225 <222> LOCATION: (1801)..(1803)
     226 <223> OTHER INFORMATION: taa stop codon.
     229 <400> SEQUENCE: 2
     231 Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
     232             -315                -310                -305
     235 Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
     236             -300                -295                -290
     239 Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
     240             -285                -280                -275
     243 Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
     244             -270                -265                -260
     247 Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
     248             -255                -250                -245
     251 Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
     252             -240                -235                -230
     255 Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
     256             -225                -220                -215
     259 Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
     260             -210                -205                -200
     263 Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
```

Delete these - they do not apply to a peptide sequence

same type of error in subsequent peptide sequences too.

RAW SEQUENCE LISTING DATE: 01/23/2006
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Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

```
264          -195                 -190                 -185
267 Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp Arg Val Thr Val  Val
268          -180                 -175                 -170
271 Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr Thr Phe Asn Asn  Ser
272          -165                 -160                 -155
275 Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile Cys Asn Leu Val  Ile
276          -150                 -145                 -140
279 Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu Pro Arg Ala Pro  Tyr
280          -135                 -130                 -125
283 Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe Arg Lys Lys Tyr  Lys
284          -120                 -115                 -110
287 Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu Glu Pro Leu Val Ala Ser
288          -105                 -100                 -95
291 His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
292          -90                  -85                  -80
295 Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
296      -75                  -70                  -65
299 Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
300 -60                  -55                  -50                  -45
303 Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
304              -40                  -35                  -30
307 Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
308          -25                  -20                  -15
311 Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
312          -10                  -5                   -1  1
315 Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
316 5                10                   15                   20
319 Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
320              25                   30                   35
323 His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
324          40                   45                   50
327 Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
328      55                   60                   65
331 Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
332  70                   75                   80
335 Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
336 85                   90                   95                   100
339 Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
340              105                  110                  115
343 Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
344          120                  125                  130
347 Thr Cys Arg
348      135
352 <210> SEQ ID NO: 3
353 <211> LENGTH: 1362
354 <212> TYPE: DNA
355 <213> ORGANISM: Ovis aries
W--> 356 <220> FEATURE:
357 <221> NAME/KEY: misc_feature
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/23/2006
PATENT APPLICATION: US/10/516,992 TIME: 09:45:14

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\01232006\J516992.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 709
Seq#:7; N Pos. 685
Seq#:13; N Pos. 685

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 47
Seq#:3; Line(s) 369
Seq#:15; Line(s) 1437

VERIFICATION SUMMARY DATE: 01/23/2006
PATENT APPLICATION: **US/10/516,992** TIME: 09:45:14

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <220> field identifier
L:39 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:63 M:283 W: Missing Blank Line separator, <220> field identifier
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:708
L:215 M:283 W: Missing Blank Line separator, <220> field identifier
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:356 M:283 W: Missing Blank Line separator, <220> field identifier
L:360 M:283 W: Missing Blank Line separator, <220> field identifier
L:363 M:283 W: Missing Blank Line separator, <220> field identifier
L:366 M:283 W: Missing Blank Line separator, <220> field identifier
L:370 M:283 W: Missing Blank Line separator, <220> field identifier
L:503 M:283 W: Missing Blank Line separator, <220> field identifier
L:507 M:283 W: Missing Blank Line separator, <220> field identifier
L:638 M:283 W: Missing Blank Line separator, <220> field identifier
L:641 M:283 W: Missing Blank Line separator, <220> field identifier
L:691 M:283 W: Missing Blank Line separator, <220> field identifier
L:694 M:283 W: Missing Blank Line separator, <220> field identifier
L:698 M:283 W: Missing Blank Line separator, <220> field identifier
L:701 M:283 W: Missing Blank Line separator, <220> field identifier
L:704 M:283 W: Missing Blank Line separator, <220> field identifier
L:708 M:283 W: Missing Blank Line separator, <220> field identifier
L:712 M:283 W: Missing Blank Line separator, <220> field identifier
L:716 M:283 W: Missing Blank Line separator, <220> field identifier
L:720 M:283 W: Missing Blank Line separator, <220> field identifier
L:723 M:283 W: Missing Blank Line separator, <220> field identifier
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:637
L:830 M:283 W: Missing Blank Line separator, <220> field identifier
L:834 M:283 W: Missing Blank Line separator, <220> field identifier
L:838 M:283 W: Missing Blank Line separator, <220> field identifier
L:842 M:283 W: Missing Blank Line separator, <220> field identifier
L:913 M:283 W: Missing Blank Line separator, <220> field identifier
L:917 M:283 W: Missing Blank Line separator, <220> field identifier
L:921 M:283 W: Missing Blank Line separator, <220> field identifier
L:924 M:283 W: Missing Blank Line separator, <220> field identifier
L:928 M:283 W: Missing Blank Line separator, <220> field identifier
L:1018 M:283 W: Missing Blank Line separator, <220> field identifier
L:1022 M:283 W: Missing Blank Line separator, <220> field identifier
L:1026 M:283 W: Missing Blank Line separator, <220> field identifier
L:1098 M:283 W: Missing Blank Line separator, <220> field identifier
L:1101 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY DATE: 01/23/2006
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Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

L:1138 M:283 W: Missing Blank Line separator, <220> field identifier
L:1141 M:283 W: Missing Blank Line separator, <220> field identifier
L:1145 M:283 W: Missing Blank Line separator, <220> field identifier
L:1148 M:283 W: Missing Blank Line separator, <220> field identifier
L:1151 M:283 W: Missing Blank Line separator, <220> field identifier
L:1155 M:283 W: Missing Blank Line separator, <220> field identifier
L:1158 M:283 W: Missing Blank Line separator, <220> field identifier
L:1162 M:283 W: Missing Blank Line separator, <220> field identifier
L:1166 M:283 W: Missing Blank Line separator, <220> field identifier
L:1169 M:283 W: Missing Blank Line separator, <220> field identifier
L:1219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:667
L:1306 M:283 W: Missing Blank Line separator, <220> field identifier
L:1310 M:283 W: Missing Blank Line separator, <220> field identifier
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L:1439 M:283 W: Missing Blank Line separator, <220> field identifier
L:1442 M:283 W: Missing Blank Line separator, <220> field identifier
L:1445 M:283 W: Missing Blank Line separator, <220> field identifier
L:1561 M:283 W: Missing Blank Line separator, <220> field identifier
L:1565 M:283 W: Missing Blank Line separator, <220> field identifier
L:1680 M:283 W: Missing Blank Line separator, <220> field identifier
L:1683 M:283 W: Missing Blank Line separator, <220> field identifier